This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS

- TEXT CUT OFF AT TOP, BOTTOM OR SIDES

- FADED TEXT

- ILLEGIBLE TEXT

- SKEWED/SLANTED IMAGES

- COLORED PHOTOS

- BLACK OR VERY BLACK AND WHITE DARK PHOTOS

- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images, please do not report the images to the Image Problem Mailbox.

NCBI   results of BLAST
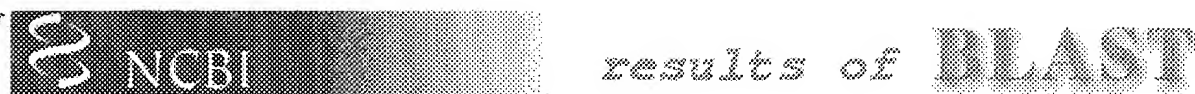
BLASTN 2.2.6 [Apr-09-2003]

RID: 1067965636-22392-2125968.BLASTQ3
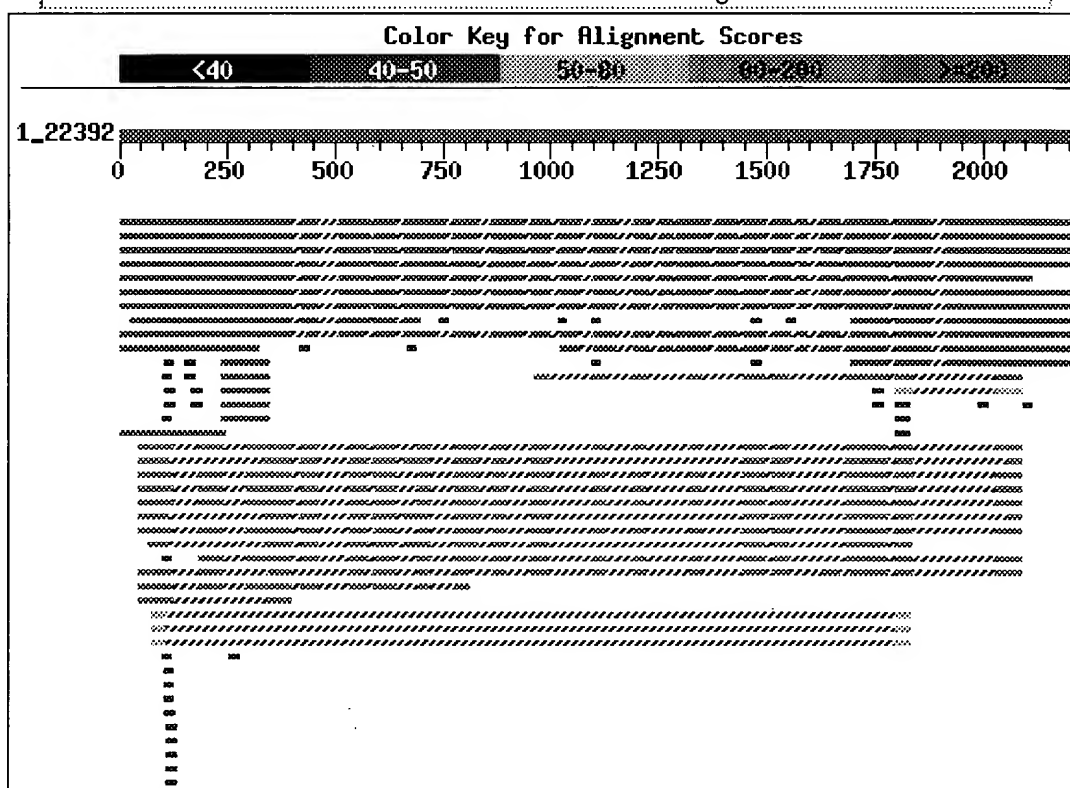
Query=   ⟋
                (2213 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
GSS, or phase 0, 1 or 2 HTGS sequences)
            1,962,268 sequences; 9,398,544,397 total letters

Taxonomy reports

Distribution of 530 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Sequences producing significant alignments:		Score (bits)	E Value	
gi|7264728|gb|AF231121.1|AF231121	Homo sapiens iron-regulat...	789	0.0	
gi|7109248|gb|AF226614.1|AF226614	Homo sapiens ferroportin1...	789	0.0	
gi|8895484|gb|AF215636.1|AF215636	Homo sapiens SLC11A3 iron...	789	0.0	

gi|23273531|gb|BC035893.1| Homo sapiens solute carrier fami...	775	0.0	
gi|12053382|emb|AL136944.1|HSM801908 Homo sapiens mRNA; cDN...	775	0.0	
gi|22902429|gb|BC037733.1| Homo sapiens solute carrier fami...	759	0.0	
gi|31543639|ref|NM_014585.3| Homo sapiens solute carrier fa...	759	0.0	
gi|33337961|gb|AF171087.1| Homo sapiens MSTP079 (MST079) mR...	704	0.0	
gi|13270751|gb|AC013439.11| Homo sapiens BAC clone RP11-270...	676	0.0	
gi|38043879|emb|AJ604512.1| Homo sapiens partial SLC40A1 ge...	628	e-176	
gi|4761673|gb|AF147322.1|AF147322 Homo sapiens full length ...	511	e-141	
gi|31873559|emb|BX537503.1|HSM805934 Homo sapiens mRNA; cDN...	504	e-139	
gi|7023677|dbj|AK002038.1| Homo sapiens cDNA FLJ11176 fis, ...	504	e-139	
gi|1034464|emb|Z62086.1|HS63B9F H.sapiens CpG island DNA ge...	228	3e-56	
gi|1028150|emb|Z56919.1|HS153B8R H.sapiens CpG island DNA g...	224	5e-55	
gi|1028149|emb|Z56918.1|HS153B8F H.sapiens CpG island DNA g...	222	2e-54	
gi|1028147|emb|Z56916.1|HS153B7F H.sapiens CpG island DNA g...	216	1e-52	
gi|1028148|emb|Z56917.1|HS153B7R H.sapiens CpG island DNA g...	210	8e-51	
gi|15880970|emb|AJ336552.1|HSA336552 Homo sapiens genomic s...	206	1e-49	
gi|8394303|ref|NM_016917.1| Mus musculus solute carrier fam...	167	1e-37	
gi|18959259|ref|NM_133315.1| Rattus norvegicus solute carri...	167	1e-37	
gi|13097389|gb|BC003438.1| Mus musculus solute carrier fami...	167	1e-37	
gi|12843053|dbj|AK008700.1| Mus musculus adult male stomach...	167	1e-37	
gi|18846873|gb|AF394785.3| Rattus norvegicus ferroportin 1 ...	167	1e-37	
gi|26328524|dbj|AK032732.1| Mus musculus 12 days embryo mal...	167	1e-37	
gi|7264726|gb|AF231120.1|AF231120 Mus musculus iron-regulat...	167	1e-37	
gi|7109246|gb|AF226613.1|AF226613 Mus musculus ferroportin1...	167	1e-37	
gi|4098298|gb|U76714.1|RRU76714 Rattus norvegicus cell adhe...	167	1e-37	
gi|8895486|gb|AF215637.1|AF215637 Mus musculus SLC11A3 iron...	167	1e-37	
gi|28933915|gb|AC123557.4| Mus musculus chromosome 1 clone ...	141	6e-30	
gi|26083702|dbj|AK033987.1| Mus musculus adult male diencep...	107	9e-20	
gi|25990284|gb|AF216834.2| Mus musculus ferroportin 1 (Slc3...	101	5e-18	
gi|26350408|dbj|AK083288.1| Mus musculus adult male liver t...	74	1e-09	
gi|18859378|ref|NM_131629.1| Danio rerio solute carrier fam...	52	0.004	
gi|19309470|emb|AL591593.11| Zebrafish DNA sequence from cl...	52	0.004	
gi|7109244|gb|AF226612.1|AF226612 Danio rerio ferroportin1 ...	52	0.004	
gi|37591194|gb|AC145321.2| Oryza sativa chromosome 11 BAC c...	46	0.27	
gi|20146016|emb|AL672145.5| Zebrafish DNA sequence from clo...	46	0.27	
gi|21998245|emb|AL731861.9| Zebrafish DNA sequence from clo...	46	0.27	
gi|21212284|emb|AL672118.8| Zebrafish DNA sequence from clo...	46	0.27	
gi|32984852|dbj|AK099643.1| Oryza sativa (japonica cultivar...	46	0.27	
gi|37651897|gb|AC146048.3| Pan troglodytes BAC clone RP43-4...	44	1.1	
gi|4508108|gb|AC005101.2| Homo sapiens BAC clone CTA-352J5 ...	44	1.1	
gi|20564430|gb|AC044786.3| Homo sapiens chromosome 10 clone...	44	1.1	
gi|15149567|emb|AL512366.12| Human DNA sequence from clone ...	44	1.1	
gi|34531610|dbj|AK125496.1| Homo sapiens cDNA FLJ43507 fis,...	44	1.1	
gi|32398496|emb|BX294670.6| Zebrafish DNA sequence from clo...	44	1.1	
gi|14329082|gb|AC011472.7|AC011472 Homo sapiens chromosome ...	44	1.1	
gi|6911646|emb|AL109865.36|HSG120K12 Human DNA sequence fro...	44	1.1	
gi|34330231|gb|AC117573.9| Mus musculus chromosome 3, clone...	42	4.3	
gi|34849934|gb|AC069562.51| Mus musculus clone rp23-317e13 ...	42	4.3	
gi|18416290|ref|NM_118549.1| Arabidopsis thaliana hypotheti...	42	4.3	
gi|28973809|gb|AC092378.4| Homo sapiens chromosome 16 clone...	42	4.3	
gi|20976936|gb|AF374874.1| Villanova achillaeoides internal...	42	4.3	

gi|4567137|gb|AF134471.1| Homo sapiens chromosome 10 clone ...   42   4.3
gi|21536172|gb|AC121772.2| Mus musculus clone RP23-349L11, ...   42   4.3
gi|21070776|gb|AC115621.3| Homo sapiens BAC clone RP11-315D...   42   4.3
gi|20514812|gb|AC012468.10| Homo sapiens chromosome 10 clon...   42   4.3
gi|23496930|gb|AE014851.1| Plasmodium falciparum 3D7 chromo...   42   4.3
gi|12666243|emb|AL354802.15| Human DNA sequence from clone ...   42   4.3
gi|26801347|gb|AC124742.4| Mus musculus chromosome 12 clone...   42   4.3
gi|15145546|gb|AC019064.6| Homo sapiens BAC clone RP11-153O...   42   4.3
gi|24413714|emb|AL939104.1|SCO939104   Streptomyces coelicolo...   42   4.3
gi|25815290|gb|AC012183.9| Homo sapiens chromosome 16 clone...   42   4.3
gi|7269265|emb|AL161561.2|ATCHRIV61   Arabidopsis thaliana DN...   42   4.3
gi|5668629|emb|AL109619.1|ATT19F6   Arabidopsis thaliana DNA ...   42   4.3
gi|16413128|emb|AL596166.1| Listeria innocua Clip11262 comp...   42   4.3
gi|11125649|emb|AL121775.3|CNS01DSG   Human chromosome 14 DNA...   42   4.3
gi|6249674|gb|AC005874.3|AC005874   citb_175_g_20, complete s...   42   4.3
gi|12484331|gb|AC021667.21|AC021667   Mus musculus, clone RP2...   42   4.3
gi|22474414|emb|AL732296.11| Mouse DNA sequence from clone ...   42   4.3
gi|9280718|gb|AC068812.13|AC068812   Homo sapiens chromosome ...   42   4.3
gi|2262097|gb|AC002343.1|ATAC002343   Arabidopsis thaliana ch...   42   4.3

Alignments

| Get selected sequences | Select all | Deselect all |

>gi|7264728|gb|AF231121.1|AF231121   Homo sapiens iron-regulated transporter
        complete cds
        Length = 2443

Score = 789 bits (398), Expect = 0.0
Identities = 398/398 (100%)
Strand = Plus / Plus

Query: 1   agctggctcagggcgtccgctaggctcggacgacctgctgagcctcccaaaccgcttcca 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1   agctggctcagggcgtccgctaggctcggacgacctgctgagcctcccaaaccgcttcca 60

Query: 61   taaggctttgctttccaacttcagctacagtgttagctaagtttggaaagaaggaaaaaa 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61   taaggctttgctttccaacttcagctacagtgttagctaagtttggaaagaaggaaaaaa 120

Query: 121 gaaaatccctgggccccttttcttttgttctttgccaaagtcgtcgttgtagtctttttg 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121 gaaaatccctgggccccttttcttttgttctttgccaaagtcgtcgttgtagtctttttg 180

Query: 181 cccaaggctgttgtgtttttagaggtgctatctccagttccttgcactcctgttaacaag 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181 cccaaggctgttgtgtttttagaggtgctatctccagttccttgcactcctgttaacaag 240

Query: 241 cacctcagcgagagcagcagcagcgatagcagccgcagaagagccagcggggtcgcctag 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241 cacctcagcgagagcagcagcagcgatagcagccgcagaagagccagcggggtcgcctag 300

```
Query: 301  tgtcatgaccagggcgggagatcacaaccgccagagaggatgctgtggatccttggccga  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301  tgtcatgaccagggcgggagatcacaaccgccagagaggatgctgtggatccttggccga  360


Query: 361  ctacctgacctctgcaaaattccttctctaccttggtc  398
             ||||||||||||||||||||||||||||||||||||||
Sbjct: 361  ctacctgacctctgcaaaattccttctctaccttggtc  398
```

 Score = 511 bits (258), Expect = e-141
 Identities = 281/290 (96%), Gaps = 9/290 (3%)
 Strand = Plus / Plus


```
Query: 1916  aatactctgggaaacaagctctttgcttgcggtcctgatgcaaaagaatttgcccaagtt  1975
             ||||||||||||||||||||||||||||||||||||||||||||||||        |||
Sbjct: 1934  aatactctgggaaacaagctctttgcttgcggtcctgatgcaaaagaa---------gtt  1984


Query: 1976  aggaaggaaaatcaagcaaatacatctgttgtttgagacagtttaactgttgctatcctg  2035
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1985  aggaaggaaaatcaagcaaatacatctgttgtttgagacagtttaactgttgctatcctg  2044


Query: 2036  ttactagattatatagagcacatgtgcttattttgtactgcagaattccaataaatggct  2095
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2045  ttactagattatatagagcacatgtgcttattttgtactgcagaattccaataaatggct  2104


Query: 2096  gggtgttttgctctgtttttaccacagctgtgccttgagaactaaaagctgtttaggaaa  2155
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2105  gggtgttttgctctgtttttaccacagctgtgccttgagaactaaaagctgtttaggaaa  2164


Query: 2156  cctaagtcagcagaaattaactgattaatttcccttatgttgaggcatgg  2205
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2165  cctaagtcagcagaaattaactgattaatttcccttatgttgaggcatgg  2214
```

 Score = 192 bits (97), Expect = 2e-45
 Identities = 97/97 (100%)
 Strand = Plus / Plus


```
Query: 1684  tgctgctagaatcggtctttggtcctttgatttaactgtgacacagttgctgcaagaaaa  1743
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1693  tgctgctagaatcggtctttggtcctttgatttaactgtgacacagttgctgcaagaaaa  1752


Query: 1744  tgtaattgaatctgaaagaggcattataaatggtgta  1780
             |||||||||||||||||||||||||||||||||||||
Sbjct: 1753  tgtaattgaatctgaaagaggcattataaatggtgta  1789
```

```
 Score =  113 bits (57), Expect = 1e-21
 Identities = 57/57 (100%)
 Strand = Plus / Plus


Query: 773 gattggattgttgttgttgcaggagaagacagaagcaaactagcaaatatgaatgcc 829
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 773 gattggattgttgttgttgcaggagaagacagaagcaaactagcaaatatgaatgcc 829



 Score =  101 bits (51), Expect = 5e-18
 Identities = 51/51 (100%)
 Strand = Plus / Plus


Query: 1445 tgtttgatcttgtgtgtgatctctgtattcatgcctggaagcccccctggac 1495
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1451 tgtttgatcttgtgtgtgatctctgtattcatgcctggaagcccccctggac 1501



 Score = 95.6 bits (48), Expect = 3e-16
 Identities = 48/48 (100%)
 Strand = Plus / Plus


Query: 1385 ggtttggttcggacaggtctgatctcaggattggcacagctttcctgt 1432
             ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1406 ggtttggttcggacaggtctgatctcaggattggcacagctttcctgt 1453



 Score = 95.6 bits (48), Expect = 3e-16
 Identities = 48/48 (100%)
 Strand = Plus / Plus


Query: 1022 aaagaagaggaaactgaattgaaacagctgaatttacacaaagatact 1069
             ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1022 aaagaagaggaaactgaattgaaacagctgaatttacacaaagatact 1069



 Score = 95.6 bits (48), Expect = 3e-16
 Identities = 48/48 (100%)
 Strand = Plus / Plus


Query: 956  tggaaggtttaccagaaaaccccagctctagctgtgaaagctggtctt 1003
             ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 974  tggaaggtttaccagaaaaccccagctctagctgtgaaagctggtctt 1021



 Score = 95.6 bits (48), Expect = 3e-16
 Identities = 48/48 (100%)
 Strand = Plus / Plus
```

```
Query: 590  ctggtggtacagaatgtttcagtcatcctgtgtggaatcatcctgatg  637
            ||||||||·|||||||||||||||||||||||||||||||||||||||||
Sbjct: 590  ctggtggtacagaatgtttcagtcatcctgtgtggaatcatcctgatg  637
```

```
 Score = 95.6 bits (48), Expect = 3e-16
 Identities = 48/48 (100%)
 Strand = Plus / Plus
```

```
Query: 530  ggtgactgggtggacaagaatgctagacttaaagtggcccagacctcg  577
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 542  ggtgactgggtggacaagaatgctagacttaaagtggcccagacctcg  589
```

```
 Score = 83.8 bits (42), Expect = 1e-12
 Identities = 42/42 (100%)
 Strand = Plus / Plus
```

```
Query: 1515  acttgtccgtttctccttttgaagatatccgatcaaggttca  1556
             ||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1500  acttgtccgtttctccttttgaagatatccgatcaaggttca  1541
```

```
 Score = 81.8 bits (41), Expect = 5e-12
 Identities = 41/41 (100%)
 Strand = Plus / Plus
```

```
Query: 1627  tgaatctgtgcccataatctctgtcagtctgctgtttgcag  1667
             |||||||||||||||||||||||||||||||||||||||||
Sbjct: 1645  tgaatctgtgcccataatctctgtcagtctgctgtttgcag  1685
```

```
 Score = 79.8 bits (40), Expect = 2e-11
 Identities = 40/40 (100%)
 Strand = Plus / Plus
```

```
Query: 1798  acagaactccatgaactatcttcttgatcttctgcatttc  1837
             ||||||||||||||||||||||||||||||||||||||||
Sbjct: 1789  acagaactccatgaactatcttcttgatcttctgcatttc  1828
```

```
 Score = 77.8 bits (39), Expect = 8e-11
 Identities = 39/39 (100%)
 Strand = Plus / Plus
```

```
Query: 419  cattctctctctacttggggagatcggatgtggcacttt  457
            |||||||||||||||||||||||||||||||||||||||
Sbjct: 398  cattctctctctacttggggagatcggatgtggcacttt  436
```

```
 Score = 73.8 bits (37), Expect = 1e-09
 Identities = 38/39 (97%)
 Strand = Plus / Plus


Query: 656 atggttttcttacataaacatgagcttctgaccatgtac 694
            ||||||||||||||||||||||||||| |||||||||||||
Sbjct: 638 atggttttcttacataaacatgarcttctgaccatgtac 676



 Score = 69.9 bits (35), Expect = 2e-08
 Identities = 35/35 (100%)
 Strand = Plus / Plus


Query: 1195 caaccagcctgtgtttctggctggcatgggtcttg 1229
             |||||||||||||||||||||||||||||||||||
Sbjct: 1213 caaccagcctgtgtttctggctggcatgggtcttg 1247



 Score = 65.9 bits (33), Expect = 3e-07
 Identities = 33/33 (100%)
 Strand = Plus / Plus


Query: 860 acaatacgaaggattgaccagttaaccaacatc 892
            |||||||||||||||||||||||||||||||||
Sbjct: 830 acaatacgaaggattgaccagttaaccaacatc 862



 Score = 60.0 bits (30), Expect = 2e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus


Query: 1295 actgtcctgggctttgactgcatcaccaca 1324
             ||||||||||||||||||||||||||||||
Sbjct: 1262 actgtcctgggctttgactgcatcaccaca 1291



 Score = 60.0 bits (30), Expect = 2e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus


Query: 1103 gagccaaaacccctggagggaactcatcta 1132
             ||||||||||||||||||||||||||||||
Sbjct: 1070 gagccaaaacccctggagggaactcatcta 1099



 Score = 48.1 bits (24), Expect = 0.069
 Identities = 24/24 (100%)
 Strand = Plus / Plus
```

```
Query: 1343 atgggaactgtagcttttacttgg 1366
             ||||||||||||||||||||||||
Sbjct: 1367 atgggaactgtagcttttacttgg 1390
```

```
 Score = 48.1 bits (24), Expect = 0.069
 Identities = 24/24 (100%)
 Strand = Plus / Plus
```

```
Query: 1325 tccatcctcagtattttgatggga 1348
             ||||||||||||||||||||||||
Sbjct: 1322 tccatcctcagtattttgatggga 1345
```

```
 Score = 46.1 bits (23), Expect = 0.27
 Identities = 23/23 (100%)
 Strand = Plus / Plus
```

```
Query: 914 tggaacttggtatccatgtgcgt 936
            |||||||||||||||||||||||
Sbjct: 935 tggaacttggtatccatgtgcgt 957
```

```
 Score = 44.1 bits (22), Expect = 1.1
 Identities = 22/22 (100%)
 Strand = Plus / Plus
```

```
Query: 716 actgcaatcacaatccaaaggg 737
            ||||||||||||||||||||||
Sbjct: 752 actgcaatcacaatccaaaggg 773
```

```
 Score = 44.1 bits (22), Expect = 1.1
 Identities = 22/22 (100%)
 Strand = Plus / Plus
```

```
Query: 695 atcctgatcatcactattgcaa 716
            ||||||||||||||||||||||
Sbjct: 704 atcctgatcatcactattgcaa 725
```

```
 Score = 44.1 bits (22), Expect = 1.1
 Identities = 22/22 (100%)
 Strand = Plus / Plus
```

```
Query: 510 tctacgggctggtggtggcagg 531
            ||||||||||||||||||||||
Sbjct: 492 tctacgggctggtggtggcagg 513
```

```
 Score = 42.1 bits (21), Expect = 4.3
 Identities = 21/21 (100%)
 Strand = Plus / Plus


Query: 1859 ggccacattatgtatttccga 1879
             |||||||||||||||||||||
Sbjct: 1904 ggccacattatgtatttccga 1924




 Score = 42.1 bits (21), Expect = 4.3
 Identities = 21/21 (100%)
 Strand = Plus / Plus


Query: 1838 gaagcttttggcttgctcgta 1858
             |||||||||||||||||||||
Sbjct: 1856 gaagcttttggcttgctcgta 1876




 Score = 42.1 bits (21), Expect = 4.3
 Identities = 21/21 (100%)
 Strand = Plus / Plus


Query: 1574 tctgctaatattgtcccggag 1594
             |||||||||||||||||||||
Sbjct: 1616 tctgctaatattgtcccggag 1636




 Score = 42.1 bits (21), Expect = 4.3
 Identities = 21/21 (100%)
 Strand = Plus / Plus


Query: 1262 gggtacgcctacactcaggga 1282
             |||||||||||||||||||||
Sbjct: 1292 gggtacgcctacactcaggga 1312




 Score = 42.1 bits (21), Expect = 4.3
 Identities = 21/21 (100%)
 Strand = Plus / Plus


Query: 1133 cttgaacatgagcaagagcct 1153
             |||||||||||||||||||||
Sbjct: 1130 cttgaacatgagcaagagcct 1150




 Score = 42.1 bits (21), Expect = 4.3
 Identities = 21/21 (100%)
 Strand = Plus / Plus
```

```
Query: 893  atgacatttggctccccagtc  913
             |||||||||||||||||||||
Sbjct: 890  atgacatttggctccccagtc  910
```

```
Score = 42.1 bits (21), Expect = 4.3
Identities = 21/21 (100%)
Strand = Plus / Plus
```

```
Query: 735  gggttctcacttcctgctata  755
             |||||||||||||||||||||
Sbjct: 684  gggttctcacttcctgctata  704
```

>gi|7109248|gb|AF226614.1|AF226614 ▓▓▓▓ Homo sapiens ferroportin1 (FPN1) mRNA, co
          Length = 2222

```
Score =  789 bits (398), Expect = 0.0
Identities = 398/398 (100%)
Strand = Plus / Plus
```

```
Query: 1    agctggctcagggcgtccgctaggctcggacgacctgctgagcctcccaaaccgcttcca  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1    agctggctcagggcgtccgctaggctcggacgacctgctgagcctcccaaaccgcttcca  60
```

```
Query: 61   taaggctttgctttccaacttcagctacagtgttagctaagtttggaaagaaggaaaaaa  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61   taaggctttgctttccaacttcagctacagtgttagctaagtttggaaagaaggaaaaaa  120
```

```
Query: 121  gaaaatccctgggccccttttcttttgttctttgccaaagtcgtcgttgtagtctttttg  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121  gaaaatccctgggccccttttcttttgttctttgccaaagtcgtcgttgtagtctttttg  180
```

```
Query: 181  cccaaggctgttgtgttttagaggtgctatctccagttccttgcactcctgttaacaag  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181  cccaaggctgttgtgttttagaggtgctatctccagttccttgcactcctgttaacaag  240
```

```
Query: 241  cacctcagcgagagcagcagcagcgatagcagccgcagaagagccagcggggtcgcctag  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241  cacctcagcgagagcagcagcagcgatagcagccgcagaagagccagcggggtcgcctag  300
```

```
Query: 301  tgtcatgaccagggcgggagatcacaaccgccagagaggatgctgtggatccttggccga  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301  tgtcatgaccagggcgggagatcacaaccgccagagaggatgctgtggatccttggccga  360
```

```
Query: 361  ctacctgacctctgcaaaattccttctctaccttggtc  398
            ||||||||||||||||||||||||||||||||||||||
Sbjct: 361  ctacctgacctctgcaaaattccttctctaccttggtc  398
```

Search [Nucleotide ▾] for [   ] [Go] [Clear]

| | Limits | Preview/Index | History | Clipboard | Details |

[Display] [default ▾] Show: [20 ▾] [Send to] [File ▾] [Get Subsequence] [Feature]

☐ **1:** <u>AF226614</u>. Homo sapiens ferr...[gi:7109248]   Links

```
LOCUS       AF226614                2222 bp    mRNA    linear   PRI 29-FEB-2000
DEFINITION  Homo sapiens ferroportin1 (FPN1) mRNA, complete cds.
ACCESSION   AF226614
VERSION     AF226614.1  GI:7109248
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2222)
  AUTHORS   Donovan,A., Brownlie,A., Zhou,Y., Shepard,J., Pratt,S.J.,
            Moynihan,J., Paw,B.H., Drejer,A., Barut,B., Zapata,A., Law,T.C.,
            Brugnara,C., Lux,S.E., Pinkus,G.S., Pinkus,J.L., Kingsley,P.D.,
            Palis,J., Fleming,M.D., Andrews,N.C. and Zon,L.I.
  TITLE     Positional cloning of zebrafish ferroportin1 identifies a conserved
            vertebrate iron exporter
  JOURNAL   Nature 403 (6771), 776-781 (2000)
  MEDLINE   20155474
   PUBMED   10693807
REFERENCE   2  (bases 1 to 2222)
  AUTHORS   Donovan,A., Brownlie,A., Shepard,J., Pratt,S.J., Paw,B.H., Barut,B.
            and Zon,L.I.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JAN-2000) Hematology/Oncology, Children's Hospital,
            300 Longwood Ave., Boston, MA 02115, USA
FEATURES             Location/Qualifiers
     source          1..2222
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /tissue_type="placenta"
     gene            1..2222
                     /gene="FPN1"
     CDS             305..2020
                     /gene="FPN1"
                     /note="transporter; iron exporter"
                     /codon_start=1
                     /product="ferroportin1"
                     /protein_id="AAF36697.1"
                     /db_xref="GI:7109249"
                     /translation="MTRAGDHNRQRGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHF
                     AVSVFLVELYGNSLLLTAVYGLVVAGSVLVLGAIIGDWVDKNARLKVAQTSLVVQNVS
                     VILCGIILMMVFLHKHELLTMYHGWVLTSCYILIITIANIANLASTATAITIQRDWIV
                     VVAGEDRSKLANMNATIRRIDQLTNILAPMAVGQIMTFGSPVIGCGFISGWNLVSMCV
                     EYVLLWKVYQKTPALAVKAGLKEEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIHEL
                     EHEQEPTCASQMAEPFRTFRDGWVSYYNQPVFLAGMGLAFLYMTVLGFDCITTGYAYT
                     QGLSGSILSILMGASAITGIMGTVAFTWLRRKCGLVRTGLISGLAQLSCLILCVISVF
```

MPGSPLDLSVSPFEDIRSRFIQGESITPTKIPEITTEIYMSNGSNSANIVPETSPESV
PIISVSLLFAGVIAARIGLWSFDLTVTQLLQENVIESERGIINGVQNSMNYLLDLLHF
IMVILAPNPEAFGLLVLISVSFVAMGHIMYFRFAQNTLGNKLFACGPDAKEVRKENQA
NTSVV"

ORIGIN
```
   1 agctggctca gggcgtccgc taggctcgga cgacctgctg agcctcccaa accgcttcca
  61 taaggctttg ctttccaact tcagctacag tgttagctaa gtttggaaag aaggaaaaaa
 121 gaaaatccct gggcccctt tcttttgttc tttgccaaag tcgtcgttgt agtcttttg
 181 cccaaggctg ttgtgttttt agaggtgcta tctccagttc cttgcactcc tgttaacaag
 241 cacctcagcg agagcagcag cagcgatagc agccgcagaa gagccagcgg ggtcgcctag
 301 tgtcatgacc agggcgggag atcacaaccg ccagagagga tgctgtggat ccttggccga
 361 ctacctgacc tctgcaaaat tccttctcta ccttggtcat tctctctcta cttggggaga
 421 tcggatgtgg cactttgcgg tgtctgtgtt tctggtagag ctctatggaa acagcctcct
 481 tttgacagca gtctacgggc tggtggtggc agggtctgtt ctggtcctgg agccatcat
 541 cggtgactgg gtggacaaga atgctagact taaagtggcc cagacctcgc tggtggtaca
 601 gaatgtttca gtcatcctgt gtggaatcat cctgatgatg gtttttcttac ataaacatga
 661 gcttctgacc atgtaccatg gatgggttct cacttcctgc tatatcctga tcatcactat
 721 tgcaaatatt gcaaatttgg ccagtactgc tactgcaatc acaatccaaa gggattggat
 781 tgttgttgtt gcaggagaag acagaagcaa actagcaaat atgaatgcca caatacgaag
 841 gattgaccag ttaaccaaca tcttagcccc catggctgtt ggccagatta tgacatttgg
 901 ctccccagtc atcggctgtg ctttatttc gggatggaac ttggtatcca tgtgcgtgga
 961 gtacgtcctg ctctggaagg tttaccagaa aaccccagct ctagctgtga aagctggtct
1021 taaagaagag gaaactgaat tgaaacagct gaatttacac aaagatactg agccaaaacc
1081 cctggaggga actcatctaa tgggtgtgaa agactctaac atccatgagc ttgaacatga
1141 gcaagagcct acttgtgcct cccagatggc tgagcccttc cgtaccttcc gagatggatg
1201 ggtctcctac tacaaccagc ctgtgtttct ggctggcatg ggtcttgctt cctttatat
1261 gactgtcctg ggctttgact gcatcaccac agggtacgcc tacactcagg gactgagtgg
1321 ttccatcctc agtattttga tgggagcatc agctataact ggaataatgg gaactgtagc
1381 ttttacttgg ctacgtcgaa aatgtggttt ggttcggaca ggtctgatct caggattggc
1441 acagctttcc tgtttgatct tgtgtgtgat ctctgtattc atgcctggaa gcccctgga
1501 cttgtccgtt tctccttttg aagatatccg atcaaggttc attcaaggag agtcaattac
1561 acctaccaag atacctgaaa ttacaactga aatatacatg tctaatgggt ctaattctgc
1621 taatattgtc ccggagacaa gtcctgaatc tgtgcccata atctctgtca gtctgctgtt
1681 tgcaggcgtc attgctgcta gaatcggtct ttggtccttt gatttaactg tgacacagtt
1741 gctgcaagaa aatgtaattg aatctgaaag aggcattata aatggtgtac agaactccat
1801 gaactatctt cttgatcttc tgcatttcat catggtcatc ctggctccaa atcctgaagc
1861 ttttggcttg ctcgtattga tttcagtctc ctttgtggca atgggccaca ttatgtattt
1921 ccgatttgcc caaaatactc tgggaaacaa gctctttgct tgcggtcctg atgcaaaaga
1981 agttaggaag gaaaatcaag caaatacatc tgttgtttga dacagtttaa ctgttgctat
2041 cctgttacta gattatatag agcacatgtg cttattttgt actgcagaat ccaataaat
2101 ggctgggtgt tttgctctgt ttttaccaca gctgtgcctt gagaactaaa agctgtttag
2161 gaaacctaag tcagcagaaa ttaactgatt aatttccctt atgttgaggc atggaaaaaa
2221 aa
```
//

Oct 29 2003 07:23:28

NCBI   results of BLAST
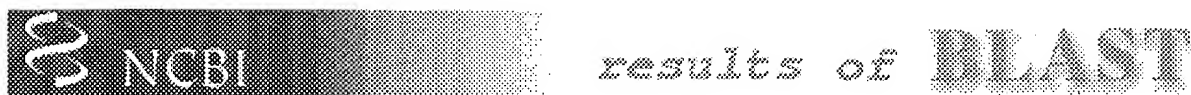
BLASTN 2.2.6 [Apr-09-2003]

RID: 1067977127-36-2085302.BLASTQ3

Query= 7 - Genomic
(7496 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)
1,962,268 sequences; 9,398,544,397 total letters

Taxonomy reports

Distribution of 211 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments
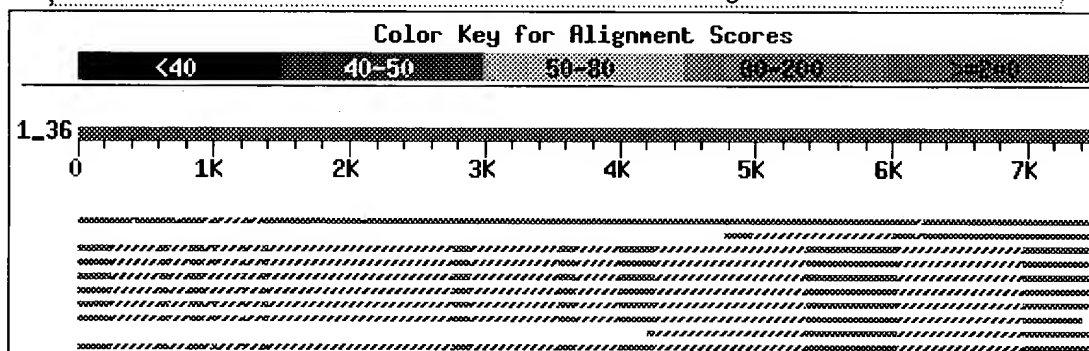
	Score (bits)	E Value	
Sequences producing significant alignments:			
gi|13270751|gb|AC013439.11| Homo sapiens BAC clone RP11-270...	2589	0.0 98	
gi|31873559|emb|BX537503.1|HSM805934 Homo sapiens mRNA; cDN...	2260	0.0 98	
gi|22902429|gb|BC037733.1| Homo sapiens solute carrier fami...	1273	0.0	
gi|31543639|ref|NM_014585.3| . Homo sapiens solute carrier fa...	1273	0.0	
gi|7109248|gb|AF226614.1|AF226614 Homo sapiens ferroportin1...	1273	0.0	
gi|12053382|emb|AL136944.1|HSM801908 Homo sapiens mRNA; cDN...	1273	0.0	
gi|23273531|gb|BC035893.1| Homo sapiens solute carrier fami...	1265	0.0	
gi|7264728|gb|AF231121.1|AF231121 Homo sapiens iron-regulat...	1265	0.0	
gi|7023677|dbj|AK002038.1| Homo sapiens cDNA FLJ11176 fis, ...	1251	0.0	
gi|8895484|gb|AF215636.1|AF215636 · Homo sapiens SLC11A3 iron...	1241	0.0	

Alignments

Get selected sequences | Select all | Deselect all

□ >gi|13270751|gb|AC013439.11| ▨ Homo sapiens BAC clone RP11-270G18 from 2, comple
          Length = 167891

 Score = 2589 bits (1306), Expect = 0.0
 Identities = 1359/1384 (98%)
 Strand = Plus / Minus

Query: 4772   gagacagagtctcgctctgttgcccaggctgaagtgcagtggcgcgatcttggctcactg 4831
              |||||||||||||||||| ||||||||||| ||||||||| |||||||||||||||||||||
Sbjct: 128831 gagacagagtctcgctctgtcgcccaggctggagtgcagtggcgcgatcttggctcactg 128772

Query: 4832   caagctctgcctcctgggttcacgccattctcctgcctcagcctcccaagtagctgggat 4891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128771 caagctctgcctcctgggttcacgccattctcctgcctcagcctcccaagtagctgggat 128712

Query: 4892   tgcaggcatccaccaccacacccggctaattttttgtattttttagtagagacggggtttc 4951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128711 tgcaggcatccaccaccacacccggctaattttttgtattttttagtagagacggggtttc 128652

Query: 4952   accatgttagccaggatggtcttgatctcctgacctcgtgatctgcccgcctcggcctcc 5011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128651 accatgttagccaggatggtcttgatctcctgacctcgtgatctgcccgcctcggcctcc 128592

Query: 5012   caaagtgctgggattacaggtgtgagccaccgtgcctggccaatacgctgtgnnnnnnna 5071
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct: 128591 caaagtgctgggattacaggtgtgagccaccgtgcctggccaatacgctgtgtttttta 128532

Query: 5072   gacaattttaatattttatctggtgagttttcctgctgtttactttggtgggagtataat 5131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128531 gacaattttaatattttatctggtgagttttcctgctgtttactttggtgggagtataat 128472

Query: 5132   ttctaagagcaagagagagagagnnnnnnnngagggatagatcaatagtattttgtttat 5191
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct: 128471 ttctaagagcaagagagagagagaaaaaaaagagggatagatcaatagtattttgtttat 128412

Query: 5192   ttaataaaaatgacacttgatgattattccttggctggaattcttagattattagtaaaa 5251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128411 ttaataaaaatgacacttgatgattattccttggctggaattcttagattattagtaaaa 128352

Query: 5252   gaaaatacatattacaatgtctaaccaagggtacccattgggaaggggaatagaaggnnn 5311
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128351 gaaaatacatattacaatgtctaaccaagggtacccattgggaaggggaatagaaggaaa 128292

Query: 5312   nnnngtactactaataattggctttttatttctacatgtcctccccaacaaaataatggta 5371
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128291 aaaagtactactaataattggctttttatttctacatgtcctccccaacaaaataatggta 128232

```
Query:  5372   tcttttcttaacagatactgagccaaaaccccttgagggaactcatctaatgggtgtgaa   5431
               |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct:  128231 tcttttcttaacagatactgagccaaaacccctggagggaactcatctaatgggtgtgaa   128172


Query:  5432   agactctaacatccatgagcttgaacatgagcaagagcctacttgtgcctcccagatggc   5491
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  128171 agactctaacatccatgagcttgaacatgagcaagagcctacttgtgcctcccagatggc   128112


Query:  5492   tgagcccttccgtaccttccgagatggatgggtctcctactacaaccagcctgtgtttct   5551
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  128111 tgagcccttccgtaccttccgagatggatgggtctcctactacaaccagcctgtgtttct   128052


Query:  5552   ggctggcatgggtcttgctttcctttatatgactgtcctgggctttgactgcatcaccac   5611
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  128051 ggctggcatgggtcttgctttcctttatatgactgtcctgggctttgactgcatcaccac   127992


Query:  5612   agggtacgcctacactcagggactgagtggttccatcctcagtattttgatgggagcatc   5671
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  127991 agggtacgcctacactcagggactgagtggttccatcctcagtattttgatgggagcatc   127932


Query:  5672   agctataactggaataatgggaactgtagcttttacttggctacgtcgaaaatgtggttt   5731
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  127931 agctataactggaataatgggaactgtagcttttacttggctacgtcgaaaatgtggttt   127872


Query:  5732   ggttcggacaggtctgatctcaggattggcacagctttcctgtttgatcttgtgtgtgat   5791
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  127871 ggttcggacaggtctgatctcaggattggcacagctttcctgtttgatcttgtgtgtgat   127812


Query:  5792   ctctgtattcatgcctggaagccccctggacttgtccgtttctccttttgaagatatccg   5851
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  127811 ctctgtattcatgcctggaagccccctggacttgtccgtttctccttttgaagatatccg   127752


Query:  5852   atcaaggttcattcaaggagagtcaattacacctaccaagatacctgaaattacaactga   5911
               |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct:  127751 atcaaggttcattcaaggagagtcaattacacctaccaagatacctgaaattacaactga   127692


Query:  5912   aatatacatgtctaatgggtctaattctgctaatattgtcccggagacaagtcctgaatc   5971
               ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  127691 aatatacatgtctaatgggtctaattctgctaatattgtcccggagacaagtcctgaatc   127632


Query:  5972   tgtgcccataatctctgtcagtctgctgtttgcaggcgtcattgctgctagaatcggtaa   6031
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  127631 tgtgcccataatctctgtcagtctgctgtttgcaggcgtcattgctgctagaatcggtaa   127572


Query:  6032   gaaatctcttttt atatattaatgaactaaagtgtcttttttgtaatgtaggttcagagaa   6091
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  127571 gaaatctcttttttatatattaatgaactaaagtgtcttttttgtaatgtaggttcagagaa   127512
```

```
Query: 6092    tccattaataaatgatctgaaatgttccctaaatgttaatttaagcaaaatccactctta 6151
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 127511 tccattaataaatgatctgaaatgttccctaaatgttaatttaagcaaaatccactctta 127452


Query: 6152    cgaa 6155
               ||||
Sbjct: 127451 cgaa 127448



 Score = 2260 bits (1140), Expect = 0.0
 Identities = 1167/1177 (99%), Gaps = 1/1177 (0%)
 Strand = Plus / Minus


Query: 6313    caaatgtcttctctagcca-tatgtatttattatatagtttgccacacaaatggatttta 6371
               |||| ||||||||||||| | ||||||||||||||||||||||||||||||||||||||||
Sbjct: 126852 caaaggtcttctctagcaaatatgtatttattatatagtttgccacacaaatggatttta 126793


Query: 6372    tagccctggaaggaaacataaagacttcttacaaagcaaaatttaagtaataattaatag 6431
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 126792 tagccctggaaggaaacataaagacttcttacaaagcaaaatttaagtaataattaatag 126733


Query: 6432    agtactgatgaattatctctgaattcagtcttgaaatgaaactgtttttatcttgtgata 6491
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 126732 agtactgatgaattatctctgaattcagtcttgaaatgaaactgtttttatcttgtgata 126673


Query: 6492    caaaacagttcattagtttattgaagatattaatttccaggcaagacagctttattgttt 6551
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 126672 caaaacagttcattagtttattgaagatattaatttccaggcaagacagctttattgttt 126613


Query: 6552    gggctttagaactctagcagtaatataacaatggtttaaagtttccttacactttaacca 6611
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 126612 gggctttagaactctagcagtaatataacaatggtttaaagtttccttacactttaacca 126553


Query: 6612    taaccatttattaggtcatttgaaacttaaaaaatactagtacttatactataataggat 6671
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 126552 taaccatttattaggtcatttgaaacttaaaaaatactagtacttatactataataggat 126493


Query: 6672    ttattatgtctctgatttcaaagttttgtttttgtagtatgaataatcacagaaaaacag 6731
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 126492 ttattatgtctctgatttcaaagttttgtttttgtagtatgaataatcacagaaaaacag 126433


Query: 6732    aactaagaagtttgtagattagacttctttttgtctgatgactgtaaaaatcatttattg 6791
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 126432 aactaagaagtttgtagattagacttctttttgtctgatgactgtaaaaatcatttattg 126373


Query: 6792    aggccactaataacccaatatttatttatgaaaaataattcttaaggcaaggctatggta 6851
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 126372 aggccactaataacccaatatttatttatgaaaaataattcttaaggcaaggctatggta 126313
```

```
Query: 6852    tatttaaggtgacttaaagacagtcaggctaaaatgtatattttgcatatgtcaacagat 6911
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 126312  tatttaaggtgacttaaagacagtcaggctaaaatgtatattttgcatatgtcaacagat 126253


Query: 6912    ttttatctgtgatttgaaatgtatgcctgtaaactaaaatctaatctttnnnnnnnntatt 6971
               |||||||||||||||||||||||||||||||||||||||||||||||||        ||||
Sbjct: 126252  ttttatctgtgatttgaaatgtatgcctgtaaactaaaatctaatctttaaaaaaatatt 126193


Query: 6972    ttattataggtctttggtcctttgatttaactgtgacacagttgctgcaagaaaatgtaa 7031
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 126192  ttattataggtctttggtcctttgatttaactgtgacacagttgctgcaagaaaatgtaa 126133


Query: 7032    ttgaatctgaaagaggcattataaatggtgtacagaactccatgaactatcttcttgatc 7091
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 126132  ttgaatctgaaagaggcattataaatggtgtacagaactccatgaactatcttcttgatc 126073


Query: 7092    ttctgcatttcatcatggtcatcctggctccaaatcctgaagcttttggcttgctcgtat 7151
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 126072  ttctgcatttcatcatggtcatcctggctccaaatcctgaagcttttggcttgctcgtat 126013


Query: 7152    tgatttcagtctcctttgtggcaatgggccacattatgtatttccgatttgcccaaaata 7211
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 126012  tgatttcagtctcctttgtggcaatgggccacattatgtatttccgatttgcccaaaata 125953


Query: 7212    ctctgggaaacaagctctttgcttgcggtcctgatgcaaaagaagttaggaaggaaaatc 7271
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 125952  ctctgggaaacaagctctttgcttgcggtcctgatgcaaaagaagttaggaaggaaaatc 125893


Query: 7272    aagcaaatacatctgttgtttgagacagtttaactgttgctatcctgttactagattata 7331
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 125892  aagcaaatacatctgttgtttgagacagtttaactgttgctatcctgttactagattata 125833


Query: 7332    tagagcacatgtgcttattttgtactgcagaattccaataaatggctgggtgttttgctc 7391
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 125832  tagagcacatgtgcttattttgtactgcagaattccaataaatggctgggtgttttgctc 125773


Query: 7392    tgtttttaccacagctgtgccttgagaactaaaagctgtttaggaaacctaagtcagcag 7451
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 125772  tgtttttaccacagctgtgccttgagaactaaaagctgtttaggaaacctaagtcagcag 125713


Query: 7452    aaattaactgattaatttcccttatgttgaggcatgg 7488
               |||||||||||||||||||||||||||||||||||||
Sbjct: 125712  aaattaactgattaatttcccttatgttgaggcatgg 125676
```

Score = 1667 bits (841), Expect = 0.0
Identities = 886/903 (98%), Gaps = 2/903 (0%)

Strand = Plus / Minus

```
Query: 2982   gagggatggggtgtggtataacccatgcatctggtgtcatattgaatcttcttgtgtata 3041
              |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct: 136399 gagggatggggtgtggtataaaccatgcatctggtgtcatattgaatcttcttgtgtata 136340


Query: 3042   tgtggattgatattatagagttgcaaagccaggtaggactttagaaatctttgagcctat 3101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 136339 tgtggattgatattatagagttgcaaagccaggtaggactttagaaatctttgagcctat 136280


Query: 3102   tcccttcattttattgaaaaaattaagacaaagtgaacgttagttgattgcccattgtca 3161
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 136279 tcccttcattttattgaaaaaattaagacaaagtgaacgttagttgattgcccattgtca 136220


Query: 3162   tgcaactagaaggtgtcagaactctgacttaaatacaggtgttttcaattccccttcaac 3221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 136219 tgcaactagaaggtgtcagaactctgacttaaatacaggtgttttcaattccccttcaac 136160


Query: 3222   attcttttcaaaggcaatatttgtgggagaaatgttcaaaaccaccactgtgttaacatt 3281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 136159 attcttttcaaaggcaatatttgtgggagaaatgttcaaaaccaccactgtgttaacatt 136100


Query: 3282   ttataactgtattcacctgactattataattttgtattatgtgtactacagatgatcta 3341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 136099 ttataactgtattcacctgactattataattttgtattatgtgtactacagatgatcta 136040


Query: 3342   gatgatacaggttaggacattatgcccattgactactggtattcattcagtttcatatct 3401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 136039 gatgatacaggttaggacattatgcccattgactactggtattcattcagtttcatatct 135980


Query: 3402   ataacgtaaaatgatttcttataaatgaaattaaaatacnnnnnnnatcattccaccaaa 3461
              |||||||||||||||||||||||||||||||||||||          ||||||||||||||
Sbjct: 135979 ataacgtaaaatgatttcttataaatgaaattaaaatacttttttttatcattccaccaaa 135920


Query: 3462   gactattttaaactgccttgtttagtgacatatgtacagtgtggtaaactgacattataa 3521
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 135919 gactattttaaactgccttgtttagtgacatatgtacagtgtggtaaactgacattataa 135860


Query: 3522   ctcannnnnnncttgtcattctttagacttcctgctatatcctgatcatcactattgcaa 3581
              ||||         |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 135859 ctcattttttcttgtcattctttagacttcctgctatatcctgatcatcactattgcaa 135800


Query: 3582   atattgcaaatttggccagtactgctactgcaatcacaatccaaagggattggattgttg 3641
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 135799 atattgcaaatttggccagtactgctactgcaatcacaatccaaagggattggattgttg 135740


Query: 3642   ttgttgcaggagaagacagaagcaaactagcaagtaatttggctttctcttttaatgaaa 3701
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct: 135739 ttgttgcaggagaagacagaagcaaactagcaagtaatttggctttctctttaatgaaa 135680


Query: 3702   tgagcatgttaggattcactttaaatcggtggtgataaatgaggctgtaag-cttgtatt 3760
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct: 135679 tgagcatgttaggattcactttaaatcggtggtgataaatgaggctgtaagccttgtatt 135620


Query: 3761   tttgttctgggtattttttaagaatgataaattgaaagcatac-ttttttcttaccttat 3819
              ||||||||||||||||||||||.|||||||||||||||||||| ||||||||||||||||
Sbjct: 135619 tttgttctgggtattttttaagaatgataaattgaaagcatactttttttcttaccttat 135560


Query: 3820   tgtcagttttagtgctgatttatctcactgttacgaagttaacttataggatagctaact 3879
              ||||||||||||.|||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 135559 tgtcagttttagtgctgatttatctcactgttacgaagttaacttataggatagctaact 135500


Query: 3880   tct 3882
              |||
Sbjct: 135499 tct 135497



 Score = 1620 bits (817), Expect = 0.0
 Identities = 844/854 (98%), Gaps = 1/854 (0%)
 Strand = Plus / Minus


Query: 3905   acattttaggaatctatactcttggtttacagctttgtattgtgtaaatgggcagtctct 3964
              ||!||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129699 acattttaggaatctatactcttggtttacagctttgtattgtgtaaatgggcagtctct 129640


Query: 3965   ctttgatgggtttgcacacttacctgcctctttcaccggcctctctagatatgaatgcca 4024
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct: 129639 ctttgatgggtttgcacacttacctgcctctttcacctgcctctctagatatgaatgcca 129580


Query: 4025   caatacgaaggattgaccagttaaccaacatcttagcccccatggctgttggccagatta 4084
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||'|||
Sbjct: 129579 caatacgaaggattgaccagttaaccaacatcttagcccccatggctgttggccagatta 129520


Query: 4085   tgacatttggctccccagtcatcggctgtggctttatttcgggatggaacttggtatcca 4144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129519 tgacatttggctccccagtcatcggctgtggctttatttcgggatggaacttggtatcca 129460


Query: 4145   tgtgcgtggagtacgtcctgctctggaaggtttaccagaaaaccccagctctagctgtga 4204
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129459 tgtgcgtggagtacgttctgctctggaaggtttaccagaaaaccccagctctagctgtga 129400


Query: 4205   aagctggtcttaaagaagaggaaactgaattgaaacagctgaatttacacaaaggtaaac 4264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129399 aagctggtcttaaagaagaggaaactgaattgaaacagctgaatttacacaaaggtaaac 129340


Query: 4265   tgaacacaatgatctctccttttgttctcatgttcagaccttaaatgttggtgaagatca 4324
```

```
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129339  tgaacacaatgatctctccttttgttctcatgttcagaccttaaatgttggtgaagatca 129280


Query: 4325   aaactattttgaatttgtatcaggtttttattaccagtgggggccagatgaggttaaatat 4384
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129279  aaactattttgaatttgtatcaggtttttattaccagtgggggccagatgaggttaaatat 129220


Query: 4385   atcgctttggtagacgaggcaagagcaggcttttgaggatctagggaaaaactccgggtt 4444
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129219  atcgctttggtagacgaggcaagagcaggcttttgaggatctagggaaaaactccgggtt 129160


Query: 4445   gaatctggtggggttagaatgggtcccctagccctcttccttgatgtgagcagtagttat 4504
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129159  gaatctggtggggttagaatgggtcccctagccctcttccttgatgtgagcagtagttat 129100


Query: 4505   agaggttcaattttacttgagagatagctgggcaaagctaagtcataggactgggaaaaa 4564
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129099  agaggttcaattttacttgagagatagctgggcaaagctaagtcataggactgggaaaaa 129040


Query: 4565   atgtggggnnnnnnngagaatgagagaatcccttggactctgtgaggagggagttatgta 4624
                     |||||||||           ||||||||||||||||||||||||||||||||||||||||
Sbjct: 129039  atgtggggaaaaaaagagaatgagagaatcccttggactctgtgaggagggagttatgta 128980


Query: 4625   gtcatttgtaggacagtggaagggagtgaggacacaaagatgggtatttcactggagaag 4684
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128979  gtcatttgtaggacagtggaagggagtgaggacacaaagatgggtatttcactggagaag 128920


Query: 4685   aggacgctgggcttctgggtaaacagaatcttttatcca-ctctgcagggacccagaaaa 4743
                     ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct: 128919  aggacgctgggcttctgggtaaacagaatcttttatccagctctgcagggacccagaaaa 128860


Query: 4744   taatatgctggttg 4757
                     ||||||||||||||
Sbjct: 128859  taatatgctggttg 128846
```

 Score = 1513 bits (763), Expect = 0.0
 Identities = 835/855 (97%), Gaps = 3/855 (0%)
 Strand = Plus / Minus

```
Query: 2116   atcatctgc-tactgag-ggcagagaaaaggctaccaggtgtctttatctgtccttactc 2173
                     |||||||||| |||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct: 137614  atcatctgcctactgagtggcagagaaaaggctaccaggtgtctttatctgtccttactc 137555


Query: 2174   cagtgctttatctatatgggcgcctcataagagagttgccatctgtgatgaaagggg-ag 2232
                     |||||||||||||||||||||||||||||||||||| ||||||||||||| |||||| ||
Sbjct: 137554  cagtgctttatctatatgggcgcctcataagagaattgccatctgtgatggaaggggtag 137495
```

```
Query: 2233   cttagaatttcgtagcaatggcaaatagcgttagtatgcaaagaaataccctgctgcttt 2292
              ||||||||||||||||||||||||||||| ||||||||||||||||||| |||||||||||
Sbjct: 137494 cttagaatttcgtagcaatggcaaatagcattagtatgcaaagaaatacactgctgcttt 137435


Query: 2293   attctgggcaaattttgtgtgtctttctatttaggtaagccatattatcagattcagc 2352
              |||||| ||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct: 137434 attcttggcaaattttgtgtgtctttctatttaggtaaaccatattatcagattcagc 137375


Query: 2353   ctgccatgtaggaggttgtaggtttgataacttcctctttaacctcatacatgttattgt 2412
              |||||||||||||||||||||.| ||| ||||||||||||||||||||||||||||||||||
Sbjct: 137374 ctgccatgtaggaggttgtagatttcataacttcctctttaacctcatacatgttattgt 137315


Query: 2413   tttaccttaagcaacaaagagctgaaatgtggatcatgtctatatcatactacagctcca 2472
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 137314 tttaccttaagcaacaaagagctgaaatgtggatcatgtctatatcatactacagctcca 137255


Query: 2473   tttatgttaaactttcaagaagataaactaaatgaaaaggtagtcattatgatagacttc 2532
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct: 137254 tttatgttaaactttcaagaagataaactaaatgaaaatgtagtcattatgatagacttc 137195


Query: 2533   agtgagcagagaagcttgtggtacttcatcatttggtttgcatatttactggtctggtgt 2592
              |||||| |||||||| ||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct: 137194 agtgaacagagaaacttgtggtacttcatcattttgtttgcatatttactggtctggtgt 137135


Query: 2593   gatcctctgggttgtattgagagtagttgaggcaggactgacttcagaaaggtttttcttt 2652
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 137134 gatcctctgggttgtattgagagtagttgaggcaggactgacttcagaaaggtttttcttt 137075


Query: 2653   ttatctggtaataattaggtctgggtattaatgtattatagtagagcaattatgtgtgga 2712
              ||||||||||||||||||||||||| |||||||||||||||||||||| |||||||||||||
Sbjct: 137074 ttatctggtaataattaggtctgtgtattaatgtattatagtagaacaattatgtgtgga 137015


Query: 2713   taagagcagtctcagtgagccatttgatgtaatgtacactttctctcttcctctgcaca 2772
              |||||| ||||||| |||| |||||||||||||||||||||||||||||||||||||||||
Sbjct: 137014 taagaacagtctcactgagacattttgatgtaatgtacactttctctcttcctctgcaca 136955


Query: 2773   gtggcccagacctcgctggtggtacagaatgtttcagtcatcctgtgtggaatcatcctg 2832
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 136954 gtggcccagacctcgctggtggtacagaatgtttcagtcatcctgtgtggaatcatcctg 136895


Query: 2833   atgatggttttcttacataaacatgagcttctgaccatgtaccatggatgggttctcgta 2892
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 136894 atgatggttttcttacataaacatgagcttctgaccatgtaccatggatgggttctcgta 136835


Query: 2893   agttctcaatgagattcttgatggcagaaaattgaatatctggtagtggtaaaggatgaa 2952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 136834 agttctcaatgagattcttgatggcagaaaattgaatatctggtagtggtaaaggatgaa 136775
```

```
Query: 2953  aatgctttgaagcta 2967
             |||||||||||||||
Sbjct: 136774 aatgctttgaagcta 136760
```

```
Score = 1324 bits (668), Expect = 0.0
Identities = 718/733 (97%), Gaps = 3/733 (0%)
Strand = Plus / Minus
```

```
Query: 1361  tcggtgactgggtggacaagaatgctagacttaaaggtgagtgttgttatataattaatc 1420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct: 139188 tcggtgactgggtggacaagaatgctagacttaaaggtgagtgttgttatataattaagc 139129
```

```
Query: 1421  cctttattcatggtaccaatgcctgagctacctctgtagcaaaggaaacaacaaactag 1480
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 139128 cctttattcatgggaccaatgcctgagctacctctgtagcaaaggaaacaacaaactag 139069
```

```
Query: 1481  gagagaaacaaccagggaatgtctgcatgccacacttgagggaggagggcttagatggca 1540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 139068 gagagaaacaaccagggaatgtctgcatgccacacttgagggaggagggcttagatggca 139009
```

```
Query: 1541  ccacctctggatggagggtcccatggctcccacacaaagttgggatgcctggacattgac 1600
             ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct: 139008 ccacctctggatggagggtcccatggctcccacacaaagttgggatgcctggacattgac 138949
```

```
Query: 1601  ctaatagannnnnnnngtatctttggctgttcataaatttcatatgttaatgattaacctt 1660
             |||||||||         |||||||||||||||||||||||||||||||||||||||||||
Sbjct: 138948 ctaatagatttttttgtatctttggctgttcataaatttcatatgttaatgattaacctt 138889
```

```
Query: 1661  gtagcacttctctgagaaccatgttaaacattaaaagtttgcttaactcaggcttcctaa 1720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 138888 gtagcacttctctgagaaccatgttaaacattaaaagtttgcttaactcaggcttcctaa 138829
```

```
Query: 1721  ctgtatcttgtactggagtccctttagtgtgatgttcctgagacagctttaacatctgtt 1780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 138828 ctgtatcttgtactggagtccctttagtgtgatgttcctgagacagctttaacatctgtt 138769
```

```
Query: 1781  ctttggttactatgtttcatgtaagagtatgtataagggaattgaaaactaagaatagct 1840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 138768 ctttggttactatgtttcatgtaagagtatgtataagggaattgaaaactaagaatagct 138709
```

```
Query: 1841  tcaaggcagaatagttgagcctggatcacaaagagctgaattataaattttgtagggaaa 1900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 138708 tcaaggcagaatagttgagcctggatcacaaagagctgaattataaattttgtagggaaa 138649
```

```
Query: 1901  aagaagaaataataatatcttgatatttattctaagcattattactgaaatcatgtcatt 1960
             ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct: 138648 aagaagaaataataatatcttgatatttattctaagcattagtactgaaatcatgtcatt 138589
```

```
Query: 1961   ttatacaggaaaagaaagtaattgatcaattaaattttttcagtatataagggaaatatgg 2020
              ||||||||| ||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct: 138588 ttatacagg-aaagaaagtaattgatcaattaaattttccagtatataagggaaatatgg 138530


Query: 2021   atgatcattcagggtaaatttttcttgaattgctcaattgataatggccaagaacctgacc 2080
              ||||||||||||||||||||||||||||||||||||||| |||||||| |||||| ||||||||
Sbjct: 138529 atgatcattcagggtaaatttttcttgaattgctcagttgataat-gccaag-acctgacc 138472


Query: 2081   atgcctgacttag 2093
              |||||||||||||
Sbjct: 138471 atgcctgacttag 138459



 Score =  347 bits (175), Expect = 2e-91
 Identities = 235/255 (92%)
 Strand = Plus / Minus


Query: 4788   ctgttgcccaggctgaagtgcagtggcgcgatcttggctcactgcaagctctgcctcctg 4847
              ||||||| |||| ||| ||||||||||| |||||||||||||||||||||||||||||||| |
Sbjct: 103947 ctgttgtccagactggagtgcagtggcacgatcttggctcactgcaagctctgcctcccg 103888


Query: 4848   ggttcacgccattctcctgcctcagcctcccaagtagctgggattgcaggcatccaccac 4907
              |||||||| ||||||||||||||||||||||||||||||| | | | |||| ||||||||
Sbjct: 103887 ggttcacaccattctcctgcctcagcctcccaagtagcttgaactacaggggcccaccac 103828


Query: 4908   cacacccggctaattttttgtattttttagtagagacggggtttcaccatgttagccagga 4967
              ||| ||||||||||||||||||||| |||||||||||||| |||||||||||||||||| |||||
Sbjct: 103827 cacgcccggctaattttttgtacttttagtagagacagggtttcaccatgttagtcagga 103768


Query: 4968   tggtcttgatctcctgacctcgtgatctgcccgcctcggcctcccaaagtgctgggatta 5027
              |||||||||||||||||||||||||||||||||||| |||||||||||||||| |||||
Sbjct: 103767 tggtcttgatctcctgacctcgtgatctgcccgcctttggcctcccaaagtgctgagatta 103708


Query: 5028   caggtgtgagccacc 5042
              |||| |||||||||||
Sbjct: 103707 caggcgtgagccacc 103693



 Score =  309 bits (156), Expect = 4e-80
 Identities = 239/266 (89%), Gaps = 3/266 (1%)
 Strand = Plus / Minus


Query: 4794   cccaggctgaagtgcagtggcgcgatcttggctcactgcaagctctgcctcctgggttca 4853
              |||||||||| ||||||||||||||||| |||| ||||||||||||||| ||| |||| ||||
Sbjct: 16531  cccaggctggagtgcagtggcgccatctcagctcactgcaagctccaccttctggattca 16472


Query: 4854   cgccattctcctgcctcagcctcccaagtagctgggattgcaggcatccaccaccacacc 4913
              |||||||||||||||||||||||||||||||||||||||||| | |||| | |||||| |||
```

```
Sbjct: 16471 cgccattctcctgcctcagcctcccaagtagctgggactacaggtgcctgccaccatacc 16412


Query: 4914  cggctaatttttttgtatttt---tagtagagacggggtttcaccatgttagccaggatgg 4970
             ||||||||||||||||||||||    ||||||||||||||||||| |||||||||||||||
Sbjct: 16411 cggctaatttttttgtattttgtttagtagagacggggtttcaccgtgttagccaggatgg 16352


Query: 4971  tcttgatctcctgacctcgtgatctgcccgcctcggcctcccaaagtgctgggattacag 5030
             |||  ||||||||||||| |||||||||| |||||||||||||||| |||||||||||||||
Sbjct: 16351 tctagatctcctgaccttgtgatctgcccacctcggcctcccatagtgctgggattacag 16292


Query: 5031  gtgtgagccaccgtgcctggccaata 5056
             | ||||||||| | ||||||||||||
Sbjct: 16291 gcgtgagccactgcgcctggccaata 16266



 Score =  283 bits (143), Expect = 2e-72
 Identities = 240/271 (88%), Gaps = 1/271 (0%)
 Strand = Plus / Minus


Query: 4772  gagacagagtctcgctctgttgcccaggctgaagtgcagtggcgcgatcttggctcactg 4831
             ||||| |||||||||| |||    |||||||||| |||||||||| | ||| |||||||
Sbjct: 132480 gagacggagtctcgctttgtcacccaggctggagtgcagtggcacagtctcaactcactg 132421


Query: 4832  caagctctgcctcctgggttcacgccattctcctgcctcagcctcccaagtagctgggat 4891
             |||||| ||||||||||||||||||||||||||||||||||||||||| |||||||| ||
Sbjct: 132420 caagctccgcctcctgggttcacgccattctcctgcctcagcctcctgagtagctgtgac 132361


Query: 4892  tgcaggcatccaccaccacacccggctaattttttt-gtattttttagtagagacggggttt 4950
             | |||||  || |||||| |||||||||||||||||| |||||||||||||||||| |||||
Sbjct: 132360 tacaggcgcccgccaccatgcccggctaatttttttgtattttttagtagagacagggttt 132301


Query: 4951  caccatgttagccaggatggtcttgatctcctgacctcgtgatctgcccgcctcggcctc 5010
             |||   ||||||||||||||| |||||||||||||||||||||||| |||||||||||||
Sbjct: 132300 cactgtgttagccaggattgtcttgatctcctgacctcgtgatccacccgcctcggcctc 132241


Query: 5011  ccaaagtgctgggattacaggtgtgagccac 5041
             ||||||||||||||||||||||| ||| |||||
Sbjct: 132240 ccaaagtgctgggattacaggcgtgggccac 132210



 Score =  266 bits (134), Expect = 5e-67
 Identities = 215/241 (89%), Gaps = 2/241 (0%)
 Strand = Plus / Plus


Query: 4775  acagagtctcgctctgttgcccaggctgaagtgcagtggcgcgatcttggctcactgcaa 4834
             ||||||||| ||||||||| |||||||||| |||||||||| | ||| ||||||||||||
Sbjct: 18535 acagagtcttgctctgtcgcccaggctggagtgcagtggcacagtctcggctcactgcaa 18594
```

```
Query:  4835   gctctgcctcctgggttcacgccattctcctgcctcagcctcccaagtagctgggattgc  4894
               | | |   | | | | | |  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |   | | | | | | | | | | |  | |
Sbjct:  18595  cctccacctcccgggttcacgccattctcctgcctcagcctcccgagtagctgggactac  18654


Query:  4895   aggcatccaccaccacacccggctaattttttgta--tttttagtagagacggggtttca  4952
               | | | |    | | | | | | | | | |  | |   | |  | | | | | | | | | | | | |    | | | | | | | | | | | | | |  | | | | | | | | |
Sbjct:  18655  aggcgcccaccaccacgcctggctaattttttgtattttttttagtagagacagggtttca  18714


Query:  4953   ccatgttagccaggatggtcttgatctcctgacctcgtgatctgcccgcctcggcctccc  5012
               | |  | | | | | | | | | | | | | | | | | | | |   | | | | | | | | | | | | |  | | | | | |    | | | | | | | | | | | | | | | |
Sbjct:  18715  ccgtgttagccaggatggtctcgatctcctgaccttgtgatccacccgcctcggcctccc  18774


Query:  5013   a 5013
               |
Sbjct:  18775  a 18775



 Score =  240 bits (121), Expect = 3e-59
 Identities = 218/248 (87%), Gaps = 3/248 (1%)
 Strand = Plus / Minus


Query:  4786   ctctgttgcccaggctgaagtgcagtggcgcgatcttggctcactgcaagctctgcctcc  4845
               | | | | | |  | | | | | | | | | | |  | |   | | | | | | | |  | |   | | | |   | | | | | | |   | | | |   | | | | | | | | | | |
Sbjct:  114321 ctctgtagcccaggctggagggcagtggtgcaatctcggctcaccgcaaactctgcctcc  114262


Query:  4846   tgggttcacgccattctcctgcctcagcctcccaagtagctgggattgcaggcatccacc  4905
               | | | | | | | |   | |   | | | | | | | | |   | | | | | | | | | | |   | | | | | | | | | | | | |   | | |   | |   | | |   |
Sbjct:  114261 tgggttcaagcgattctcctgtctcagcctcccgagtagctgggattacagtcacccatc  114202


Query:  4906   accacacccggctaattttttgtattttttagtagagacggggtttcaccatgttagccag  4965
               | |   |   | | |   | | | | | |   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |   | | | | |
Sbjct:  114201 acaaaacctggctaa-tttttgtattttttagtagagacggggtttcaccatgttggccag  114143


Query:  4966   gatggtcttgatctcctgacctc--gtgatctgcccgcctcggcctcccaaagtgctggg  5023
               | | | | | |   | |   | | | | | | | | | | |    | | | | | |   | | |   | | | | | | | | | | | | |   | | | | | | | | | |
Sbjct:  114142 tctggtctcgaactcctgacctcaggtgatccgcctgcctcggcctcctaaagtgctggg  114083


Query:  5024   attacagg 5031
               | | | | | | | |
Sbjct:  114082 attacagg 114075



 Score =  238 bits (120), Expect = 1e-58
 Identities = 229/263 (87%), Gaps = 3/263 (1%)
 Strand = Plus / Plus


Query:  4793   gcccaggctgaagtgcagtggcgcgatcttggctcactgcaagctctgcctcctgggttc  4852
               | | | | | | |   | |   | |   | | |   | | | | | | | | | |   | | | | | | | | | | | | | |   | | |   | | | | | | | | | | | | |
Sbjct:  109018 gcccaggttggagagcaatggcgcgatttcggctcactgcaacctccgcctcctgggttc  109077
```

```
Query: 4853    acgccattctcctgcctcagcctcccaagtagctgggattgcaggcatccaccaccacac 4912
               | || ||||||| |||||||||||||| ||||||||||||| ||||    |||||||||| |
Sbjct: 109078  aagcaattctcttgcctcagcctccctagtagctgggattacaggtgcccaccaccacgc 109137


Query: 4913    ccggctaattttttgtattttagtagagacggggtttcaccatgttagccaggatggtc 4972
               || ||||| ||||||||||| ||||||||| ||||||||||||||||| |||||| |||||
Sbjct: 109138  ccagctaa-tttttgtattttcagtagagatggggtttcaccatgttggccaggctggtc 109196


Query: 4973    ttgatctcctgacctc--gtgatctgcccgcctcggcctcccaaagtgctgggattacag 5030
               | || |||||||||||   ||||||  |||||||||||||||||||||||||||||||||||
Sbjct: 109197  tcgaactcctgacctcaggtgatccacccgcctcggcctcccaaagtgctgggattacag 109256


Query: 5031    gtgtgagccaccgtgcctggcca 5053
               |||||| ||||| | ||||||||
Sbjct: 109257  ccgtgagctaccgcgactggcca 109279



 Score =  238 bits (120), Expect = 1e-58
 Identities = 230/264 (87%), Gaps = 2/264 (0%)
 Strand = Plus / Plus


Query: 4778    gagtctcgctctgttgcccaggctgaagtgcagtggcgcgatcttggctcactgcaagct 4837
               |||||||  ||||| |||||||||||  ||| |||||||  |||||  |||||||||||  ||
Sbjct: 89758   gagtctcactctgtcgcccaggctggagttcagtggcacgatcctggctcactgcagcct 89817


Query: 4838    ctgcctcctgggttcacgccattctcctgcctcagcctcccaagtagct-gggattgcag 4896
               |  |||||||||||  || ||||||||||||||||||||||||||||||| ||||    |||
Sbjct: 89818   ccacctcctgggttcaagctattctcctgcctcagcctcccaagtagcttgggaccacag 89877


Query: 4897    gcatccaccaccacacccggctaattttttgtattttagtagagacggggtttcaccat 4956
               ||||||||| ||| |||||||||||||||| ||||||||||||||||||| ||||||||||
Sbjct: 89878   ctgcgcaccaccacgcccagctaatttttt-gtattttagtagagacgggatttcaccat 89936


Query: 4957    gttagccaggatggtcttgatctcctgacctcgtgatctgcccgcctcggcctcccaaag 5016
               ||| ||||||||||| ||||||||||||| || ||||||| | | |||| ||||||||||||
Sbjct: 89937   gttggccaggatggccttgatctcctgatcttgtgatccgtctgccttggcctcccaaag 89996


Query: 5017    tgctgggattacaggtgtgagcca 5040
               ||||||||||||||| |||||||||
Sbjct: 89997   tgctgggattacaggcgtgagcca 90020



 Score =  218 bits (110), Expect = 1e-52
 Identities = 233/272 (85%), Gaps = 9/272 (3%)
 Strand = Plus / Plus


Query: 4772    gagacagagtctcgctctgttgcccaggctgaagtgcagtggcgcgatcttggctcactg 4831
```

```
           ||||| |||||||||||||||    |||||||| ||||||||||||     ||| ||||||||||
Sbjct: 67149 gagacggagtctcgctctgtcttccaggctggagtgcagtgg-----tctcggctcactg 67203


Query: 4832   caagctctgcctcctgggttcacgccattctcctgcctcagcctcccaagtagctgggat 4891
              ||| ||| |||||| |||| || |   |||    |||||||||||||||| |||||| ||||||
Sbjct: 67204 caacctccgcctcccgggtgcaagagatt---ctgcctcagcctcccgagtagttgggat 67260


Query: 4892   tgcaggcatccaccaccacacccggctaa-ttttttgtattttttagtagagacggggttt 4950
              |||||||| | |||| |||| |||||||| ||||||||||||||||||||||||||||||||
Sbjct: 67261 tgcaggcacgcgccactacactcggctaattttttttgtattttttagtagagacggggttt 67320


Query: 4951   caccatgttagccaggatggtcttgatctcctgacctcgtgatctgcccgcctcggcctc 5010
              |||   |||||||||||||||||||||  |||||||||||||||| ||| ||||||||| |||||
Sbjct: 67321 cacggtgttagccaggatggtctccatctcctgacctcgtaatccgcccgcctctgcctc 67380


Query: 5011   ccaaagtgctgggattacaggtgtgagccacc 5042
              |||||| || |||||||||||| |||||||||||
Sbjct: 67381 ccaaagcgccgggattacaggcgtgagccacc 67412



 Score =  218 bits (110), Expect = 1e-52
 Identities = 202/229 (88%), Gaps = 4/229 (1%)
 Strand = Plus / Minus


Query: 4815   gcgatcttggctcactgcaagctctgcctcctgggttcacgccattctcctgcctcagcc 4874
              ||||||| |||||||||||| |||||||||| | |||||| |  ||||||||| ||||||
Sbjct: 21189 gcgatctcggctcactgcaaactctgcctcccgagttcaagtgattctcctgcttcagcc 21130


Query: 4875   tcccaagtagctgggattgcaggcatccaccaccacacccggctaattttttgtatttttt 4934
              ||||||||||||||||||| |||||| | ||||||| || |||||| ||||||||||||| |
Sbjct: 21129 tcccaagtagctgggattacaggcacctaccaccacgcctggctaa-tttttgtatttct 21071
```
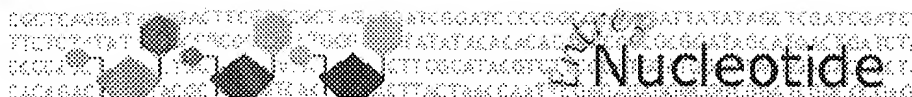
☐ **1: AF231121.** Homo sapiens iron...[gi:7264728]   Links

```
LOCUS       AF231121                2443 bp    mRNA    linear   PRI 20-MAR-2000
DEFINITION  Homo sapiens iron-regulated transporter IREG1 (IREG1) mRNA,
            complete cds.
ACCESSION   AF231121
VERSION     AF231121.1  GI:7264728
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2443)
  AUTHORS   McKie,A.T., Marciani,P., Rolfs,A., Brennan,K., Wehr,K., Barrow,D.,
            Miret,S., Bomford,A., Peters,T.J., Farzaneh,F., Hediger,M.A.,
            Hentze,M.W. and Simpson,R.J.
  TITLE     A novel duodenal iron-regulated transporter, IREG1, implicated in
            the basolateral transfer of iron to the circulation
  JOURNAL   Mol. Cell 5 (2), 299-309 (2000)
  MEDLINE   20337919
   PUBMED   10882071
REFERENCE   2  (bases 1 to 2443)
  AUTHORS   McKie,A.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-FEB-2000) Molecular Medicine, King's College London,
            Guy's, King's and St. Thomas' Medical School, Rayne Institute 123
            Coldharbour Lane, London SE5 9NU, UK
FEATURES             Location/Qualifiers
     source          1..2443
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="2"
     gene            1..2443
                     /gene="IREG1"
     misc_feature    72..110
                     /gene="IREG1"
                     /note="iron responsive element IRE"
     CDS             305..2020
                     /gene="IREG1"
                     /note="basolateral membrane protein involved in iron
                     transport; highly expressed in duodenal mucosa;
                     up-regulated in hereditary haemochromatosis"
                     /codon_start=1
                     /product="iron-regulated transporter IREG1"
                     /protein_id="AAF44330.1"
                     /db_xref="GI:7264729"
                     /translation="MTRAGDHNRQRGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHF
                     AVSVFLVELYGNSLLLTAVYGLVVAGSVLVLGAIIGDWVDKNARLKVAQTSLVVQNVS
                     VILCGIILMMVFLHKHELLTMYHGWVLTSCYILIITIANIANLASTATAITIQRDWIV
```

VVAGEDRSKLANMNATIRRIDQLTNILAPMAVGQIMTFGSPVIGCGFISGWNLVSMCV
EYVLLWKVYQKTPALAVKAGLKEEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIHEL
EHEQEPTCASQMAEPFRTFRDGWVSYYNQPVFLAGMGLAFLYMTVLGFDCITTGYAYT
QGLSGSILSILMGASAITGIMGTVAFTWLRRKCGLVRTGLISGLAQLSCLILCVISVF
MPGSPLDLSVSPFEDIRSRFIQGESITPTKIPEITTEIYMSNGSNSANIVPETSPESV
PIISVSLLFAGVIAARIGLWSFDLTVTQLLQENVIESERGIINGVQNSMNYLLDLLHF
IMVILAPNPEAFGLLVLISVSFVAMGHIMYFRFAQNTLGNKLFACGPDAKEVRKENQA
NTSVV"

ORIGIN
```
      1 agctggctca gggcgtccgc taggctcgga cgacctgctg agcctcccaa accgcttcca
     61 taaggctttg ctttccaact tcagctacag tgttagctaa gtttggaaag aaggaaaaaa
    121 gaaaatccct gggccccttt tcttttgttc tttgccaaag tcgtcgttgt agtctttttg
    181 cccaaggctg ttgtgttttt agaggtgcta tctccagttc cttgcactcc tgttaacaag
    241 cacctcagcg agagcagcag cagcgatagc agccgcagaa gagccagcgg ggtcgcctag
    301 tgtcatgacc agggcgggag atcacaaccg ccagagagga tgctgtggat ccttggccga
    361 ctacctgacc tctgcaaaat tccttctcta ccttggtcat tctctctcta cttggggaga
    421 tcggatgtgg cactttgcgg tgtctgtgtt tctggtagag ctctatggaa acagcctcct
    481 tttgacagca gtctacgggc tggtggtggc agggtctgtt ctggtcctgg gagccatcat
    541 cggtgactgg gtggacaaga atgctagact taaagtggcc cagacctcgc tggtggtaca
    601 gaatgtttca gtcatcctgt gtggaatcat cctgatgatg gttttcttac ataaacatga
    661 rcttctgacc atgtaccatg gatgggttct cacttcctgc tatatcctga tcatcactat
    721 tgcaaatatt gcaaatttgg ccagtactgc tactgcaatc acaatccaaa gggattggat
    781 tgttgttgtt gcaggagaag acagaagcaa actagcaaat atgaatgcca caatacgaag
    841 gattgaccag ttaaccaaca tcttagcccc catggctgtt ggccagatta tgacatttgg
    901 ctccccagtc atcggctgtg gctttatttc gggatggaac ttggtatcca tgtgcgtgga
    961 gtacgtcctg ctctggaagg tttaccagaa aaccccagct ctagctgtga aagctggtct
   1021 taaagaagag gaaactgaat tgaaacagct gaatttacac aaagatactg agccaaaacc
   1081 cctggaggga actcatctaa tgggtgtgaa ggactctaac atccatgagc ttgaacatga
   1141 gcaagagcct acttgtgcct cccagatggc tgagcccttc cgtaccttcc gagatggatg
   1201 ggtctcctac tacaaccagc ctgtgtttct ggctggcatg ggtcttgctt tcctttatat
   1261 gactgtcctg ggctttgact gcatcaccac agggtacgcc tacactcagg gactgagtgg
   1321 ttccatcctc agtattttga tgggagcatc agctataact ggaataatgg gaactgtagc
   1381 ttttacttgg ctacgtcgaa aatgtggttt ggttcggaca ggtctgatct caggattggc
   1441 acagctttcc tgtttgatct tgtgtgtgat ctctgtattc atgcctggaa gccccctgga
   1501 cttgtccgtt tctccttttg aagatatccg atcaaggttc attcaaggag agtcaattac
   1561 acctaccaag atacctgaaa ttacaactga aatatacatg tctaatgggt ctaattctgc
   1621 taatattgtc ccggagacaa gtcctgaatc tgtgcccata atctctgtca gtctgctgtt
   1681 tgcaggcgtc attgctgcta gaatcggtct ttggtccttt gatttaactg tgacacagtt
   1741 gctgcaagaa aatgtaattg aatctgaaag aggcattata aatggtgtac agaactccat
   1801 gaactatctt cttgatcttc tgcatttcat catggtcatc ctggctccaa atcctgaagc
   1861 ttttggcttg ctcgtattga tttcagtctc ctttgtggca atgggccaca ttatgtattt
   1921 ccgatttgcc caaaatactc tgggaaacaa gctctttgct tgcggtcctg atgcaaaaga
   1981 agttaggaag gaaaatcaag caaatacatc tgttgtttga gacagtttaa ctgttgctat
   2041 cctgttacta gattatatag agcacatgtg cttattttgt actgcagaat ccaataaat
   2101 ggctgggtgt tttgctctgt ttttaccaca gctgtgcctt gagaactaaa agctgtttag
   2161 gaaacctaag tcagcagaaa ttaactgatt aatttccctt atgttgaggc atggraaaaa
   2221 aattggraaa aggaaaaact cagttttaaa tacgggagac tataatggat aacactgrat
   2281 tcccctattt ctcatgagta gatacaatct tacgtaaaag agtggttagt cacgtgaatt
   2341 cagttatcat ttgacagatt cttatctgta ctagaattca gatatgtcag ttttctgcaa
   2401 aactcactct tgttcaagac tagctaattt attttttgc atc
```
//